

295199US0PCT.ST25.txt
SEQUENCE LISTING

<110> Endo, Keiji
Ozaki, Katsuya

<120> Modified promoter

<130> 295199US0PCT

<140> 10/589,960

<141> 2006-08-18

<150> PCT/JP05/03757

<151> 2006-03-04

<150> JP 2004-062853

<151> 2004-03-05

<160> 20

<170> PatentIn version 3.3

<210> 1

<211> 572

<212> DNA

<213> Bacillus sp. KSM-S237

<400> 1

gatttgcgcga tgcaacaggc ttatatttagt agggaaatttc tttttaaattt gaatacggaa 60

taaaatcagg taaacagggtc ctgattttat ttttttgagt ttttttagaga actgaagatt 120

gaaataaaaag tagaagacaa aggacataag aaaatttgcatt tagtttaat tataaaaaac 180

gcctttttat aattattttat acctagaacg aaaatactgt ttgcggaaagcg gtttactata 240

aaacccttata ttccggctct tttttaaaac aggggttaaa aattcactct agtattctaa 300

tttcaacatg ctataataaa tttgtaagac gcaatatgca tctttttt tacgatataat 360

gtaagcgggtt aaccttggtgc tataatgcga ttttaggaagg ggggttagatt gagtcaagta 420

gtaataatat agataactta taagttgttg agaagcagga gagcatctgg gttactcaca 480

agttttttta aaactttaac gaaagcactt tcggtaatgc ttatgaattt agctatttga 540

ttcaattact taaaaat ttaggaggtt at 572

<210> 2

<211> 609

<212> DNA

<213> Bacillus sp. KSM-64

<400> 2

agtacttacc attttagagt caaaagatag aagccaagca ggatttgccg atgcaaccgg 60

cttatattta gagggatattt ctttttaat tgaatacggta ataaaatcag gtaaacaggt 120

cctgattttta ttttttgaa ttttttgag aactaaagat tgaaatagaa gtagaagaca 180

acggacataaa gaaaattgtt ttagtttaa ttatagaaaa cgctttctta taattattta 240

295199US0PCT.ST25.txt

tacctagaac	gaaaatactg	tttcgaaagc	ggtttactat	aaaaccttat	attccggctc	300
ttttttaaa	cagggggtga	aaattcactc	tagtattcta	atttcaacat	gctataataa	360
atttgtaaga	cgcaatatac	atctttttt	tatgatattt	gtaagcggtt	aaccttgc	420
tatatgccga	tttaggaagg	gggttagattg	agtcaagtag	tcataattt	gataacttat	480
aagttgtga	gaagcaggag	agaatctggg	ttactcacaa	gtttttaaa	acattatcga	540
aagcactttc	ggttatgctt	atgaatttag	ctatttgatt	caattacttt	aataatttt	600
ggaggtaat						609
<210>	3					
<211>	3149					
<212>	DNA					
<213>	Bacillus sp. KSM-S237					
<400>	3					
gattgccga	tgcaacaggc	ttatatttag	aggaaatttc	tttttaaatt	gaatacggaa	60
taaaatcagg	taaacaggc	ctgattttat	tttttgagt	tttttagaga	actgaagatt	120
gaaataaaaag	tagaagacaa	aggacataag	aaaattgcat	tagtttaat	tatagaaaac	180
gccttttat	aattatttat	acctagaacg	aaaatactgt	ttcgaaagcg	gtttactata	240
aaaccttata	ttccggctct	ttttaaaac	agggggtaaa	aattcactct	agtattctaa	300
tttcaacatg	ctataataaa	tttgaagac	gcaatatgca	tctttttt	tacgatata	360
gtaagcggtt	aaccttgc	tatatgccga	tttaggaagg	ggggtagatt	gagtcaagta	420
gtaataatat	agataactta	taagttgtt	agaagcagga	gagcatctgg	gttactcaca	480
agtttttta	aaactttaac	gaaagcactt	tcggtaatgc	ttatgaattt	agctatttga	540
ttcaattact	ttaaaaat	tttaggagta	atatgtgtt	agaaagaaaa	caaagcagtt	600
gatttcttcc	attcttattt	tagtttact	tctatctta	tttccggcag	ctcttcagc	660
agaaggaaac	actcgtaag	acaattttaa	acatttatta	ggtaatgaca	atgttaaacg	720
cccttctgag	gctggcgc	tacaattaca	agaagtcgt	ggacaaatga	cattagtaga	780
tcaacatgga	gaaaaattc	aattacgtgg	aatgagtaca	cacggattac	agtggtttcc	840
tgagatctt	aatgataacg	catacaaagc	tctttcta	gattgggatt	ccaatatgat	900
tcgtcttgct	atgtatgt	gtaaaaatgg	gtacgctaca	aaccctgagt	taatcaaaca	960
aagagtgatt	gatggaaattt	agttagcgt	tgaaaatgac	atgtatgtt	ttgttgactg	1020
gcatgttcat	gcgccagg	atccataga	tcctgtttat	gcaggtgcta	aagatttctt	1080
tagagaaatt	gcagctt	accctaataa	tccacacatt	atttatgagt	tagcgaatga	1140
gccgagtagt	aataataatg	gtggagcagg	gattccgaat	aacgaagaag	gttgaaagc	1200
ggtaaaagaa	tatgctgatc	caattgtaga	aatgttacgt	aaaagcggta	atgcagatga	1260

295199US0PCT.ST25.txt

caacattatc attgttggta gtccaaactg gagtcagcgt ccggacttag cagctgataa	1320
tccaaattgat gatcaccata caatgtatac tgttcacttc tacactggtt cacatgctgc	1380
ttcaactgaa agctatccgt ctgaaaactcc taactctgaa agaggaaacg taatgagtaa	1440
cactcgttat gcgttagaaa acggagtagc ggtatttgc acagagtggg gaacgagtca	1500
agcttagtggaa gacggtggtc cttactttga tgaagcagat gtatggattt aattttaaa	1560
tgaaaacaac attagctggg ctaactggc tttaacgaat aaaaatgaag tatctggtgc	1620
atttacacca ttcgagttag gtaagtctaa cgcaaccaat cttgacccag gtccagatca	1680
tgtgtggca ccagaagaat taagtcttc tggagaatat gtacgtgctc gtattaaagg	1740
tgtgaactat gagccaatcg accgtacaaa atacacgaaa gtactttggg actttaatga	1800
tggAACGAAG caaggatttg gagtgaattc ggattctcca aataaagaac ttattgcagt	1860
tgataatgaa aacaacactt tgaaagttc gggatttagat gtaagtaacg atgtttcaga	1920
tggcaacttc tgggctaattc ctcgtcttc tgccaaacggt tggggaaaaaa gtgttgat	1980
tttaggtgct gagaagctta caatggatgt tattgttgat gaaccaacga cggtagctat	2040
tgcggcgatt ccacaaagta gtaaaagtgg atgggcaaatt ccagagcgtg ctgttcgagt	2100
gaacgcggaa gattttgtcc agcaaacgga cggtaaatgat aaagctggat taacaattac	2160
aggagaagat gctcctaacc taaaaaatat cgctttcat gaagaagata acaatatgaa	2220
caacatcatt ctgttcgtgg gaactgatgc agctgacgat atttacttag ataacattaa	2280
agtaattgga acagaagttg aaattccagt tgttcatgat cccaaaggag aagctgttct	2340
tccttctgtt tttgaagacg gtacacgtca aggttggac tgggctggag agtctgggt	2400
gaaaacagct ttaacaattt aagaagcaaa cggttctaacc gcgttatcat gggaaatttgg	2460
atatccagaa gtaaaaccta gtgataactg ggcaacagct ccacgttttag atttctggaa	2520
atctgacttg gttcgccgtg agaatgatta tttttttt gatttctatc tagatccagt	2580
tcgtgcaaca gaaggcgca tgaatatcaa ttttagtattc cagccaccta ctaacggta	2640
ttgggtacaa gcacaaaaaa cgtatacgat taactttgat gaatttagagg aagcgaatca	2700
agtaaatggt ttatatcact atgaagtggaa aattaacgta agagatatta caaacattca	2760
agatgacacg ttactacgta acatgatgat cattttgca gatgttagaaa gtgactttgc	2820
agggagagtc tttttttttagata atgttcgttt tgagggggct gctactactg agccgggt	2880
accagagcca gttgatccgt gcgaagagac gccacctgat gatgagaagg aagcgaaaaaa	2940
agaacaaaaaa gaagcagaga aagaagagaa agaagcagta aaagaagaaaa agaaagaagc	3000
taaagaagaa aagaaagcag tcaaaaatga ggctaagaaaa aaataatcta ttaaactagt	3060
tatagggta tctaaaggcgt tgatgttagat ctttttagata accttttct tgcataactg	3120
gacacagagt tgtttattaaa gaaagtaag	3149

295199US0PCT.ST25.txt

<210> 4
<211> 795
<212> PRT
<213> *Bacillus* sp. KSM-S237

<400> 4

Ala Glu Gly Asn Thr Arg Glu Asp Asn Phe Lys His Leu Leu Gly Asn
1 5 10 15

Asp Asn Val Lys Arg Pro Ser Glu Ala Gly Ala Leu Gln Leu Gln Glu
20 25 30

Val Asp Gly Gln Met Thr Leu Val Asp Gln His Gly Glu Lys Ile Gln
35 40 45

Leu Arg Gly Met Ser Thr His Gly Leu Gln Trp Phe Pro Glu Ile Leu
50 55 60

Asn Asp Asn Ala Tyr Lys Ala Leu Ser Asn Asp Trp Asp Ser Asn Met
65 70 75 80

Ile Arg Leu Ala Met Tyr Val Gly Glu Asn Gly Tyr Ala Thr Asn Pro
85 90 95

Glu Leu Ile Lys Gln Arg Val Ile Asp Gly Ile Glu Leu Ala Ile Glu
100 105 110

Asn Asp Met Tyr Val Ile Val Asp Trp His Val His Ala Pro Gly Asp
115 120 125

Pro Arg Asp Pro Val Tyr Ala Gly Ala Lys Asp Phe Phe Arg Glu Ile
130 135 140

Ala Ala Leu Tyr Pro Asn Asn Pro His Ile Ile Tyr Glu Leu Ala Asn
145 150 155 160

Glu Pro Ser Ser Asn Asn Asn Gly Gly Ala Gly Ile Pro Asn Asn Glu
165 170 175

Glu Gly Trp Lys Ala Val Lys Glu Tyr Ala Asp Pro Ile Val Glu Met
180 185 190

Leu Arg Lys Ser Gly Asn Ala Asp Asp Asn Ile Ile Ile Val Gly Ser
195 200 205

Pro Asn Trp Ser Gln Arg Pro Asp Leu Ala Ala Asp Asn Pro Ile Asp
210 215 220

295199US0PCT.ST25.txt

Asp His His Thr Met Tyr Thr Val His Phe Tyr Thr Gly Ser His Ala
225 230 235 240

Ala Ser Thr Glu Ser Tyr Pro Ser Glu Thr Pro Asn Ser Glu Arg Gly
245 250 255

Asn Val Met Ser Asn Thr Arg Tyr Ala Leu Glu Asn Gly Val Ala Val
260 265 270

Phe Ala Thr Glu Trp Gly Thr Ser Gln Ala Ser Gly Asp Gly Gly Pro
275 280 285

Tyr Phe Asp Glu Ala Asp Val Trp Ile Glu Phe Leu Asn Glu Asn Asn
290 295 300

Ile Ser Trp Ala Asn Trp Ser Leu Thr Asn Lys Asn Glu Val Ser Gly
305 310 315 320

Ala Phe Thr Pro Phe Glu Leu Gly Lys Ser Asn Ala Thr Asn Leu Asp
325 330 335

Pro Gly Pro Asp His Val Trp Ala Pro Glu Glu Leu Ser Leu Ser Gly
340 345 350

Glu Tyr Val Arg Ala Arg Ile Lys Gly Val Asn Tyr Glu Pro Ile Asp
355 360 365

Arg Thr Lys Tyr Thr Lys Val Leu Trp Asp Phe Asn Asp Gly Thr Lys
370 375 380

Gln Gly Phe Gly Val Asn Ser Asp Ser Pro Asn Lys Glu Leu Ile Ala
385 390 395 400

Val Asp Asn Glu Asn Asn Thr Leu Lys Val Ser Gly Leu Asp Val Ser
405 410 415

Asn Asp Val Ser Asp Gly Asn Phe Trp Ala Asn Ala Arg Leu Ser Ala
420 425 430

Asn Gly Trp Gly Lys Ser Val Asp Ile Leu Gly Ala Glu Lys Leu Thr
435 440 445

Met Asp Val Ile Val Asp Glu Pro Thr Thr Val Ala Ile Ala Ala Ile
450 455 460

Pro Gln Ser Ser Lys Ser Gly Trp Ala Asn Pro Glu Arg Ala Val Arg

465

470

475

480

Val Asn Ala Glu Asp Phe Val Gln Gln Thr Asp Gly Lys Tyr Lys Ala
485 490 495

Gly Leu Thr Ile Thr Gly Glu Asp Ala Pro Asn Leu Lys Asn Ile Ala
500 505 510

Phe His Glu Glu Asp Asn Asn Met Asn Asn Ile Ile Leu Phe Val Gly
515 520 525

Thr Asp Ala Ala Asp Val Ile Tyr Leu Asp Asn Ile Lys Val Ile Gly
530 535 540

Thr Glu Val Glu Ile Pro Val Val His Asp Pro Lys Gly Glu Ala Val
545 550 555 560

Leu Pro Ser Val Phe Glu Asp Gly Thr Arg Gln Gly Trp Asp Trp Ala
565 570 575

Gly Glu Ser Gly Val Lys Thr Ala Leu Thr Ile Glu Glu Ala Asn Gly
580 585 590

Ser Asn Ala Leu Ser Trp Glu Phe Gly Tyr Pro Glu Val Lys Pro Ser
595 600 605

Asp Asn Trp Ala Thr Ala Pro Arg Leu Asp Phe Trp Lys Ser Asp Leu
610 615 620

Val Arg Gly Glu Asn Asp Tyr Val Ala Phe Asp Phe Tyr Leu Asp Pro
625 630 635 640

Val Arg Ala Thr Glu Gly Ala Met Asn Ile Asn Leu Val Phe Gln Pro
645 650 655

Pro Thr Asn Gly Tyr Trp Val Gln Ala Pro Lys Thr Tyr Thr Ile Asn
660 665 670

Phe Asp Glu Leu Glu Glu Ala Asn Gln Val Asn Gly Leu Tyr His Tyr
675 680 685

Glu Val Lys Ile Asn Val Arg Asp Ile Thr Asn Ile Gln Asp Asp Thr
690 695 700

Leu Leu Arg Asn Met Met Ile Ile Phe Ala Asp Val Glu Ser Asp Phe
705 710 715 720

Ala Gly Arg Val Phe Val Asp Asn Val Arg Phe Glu Gly Ala Ala Thr
 725 730 735

Thr Glu Pro Val Glu Pro Glu Pro Val Asp Pro Gly Glu Glu Thr Pro
 740 745 750

Pro Val Asp Glu Lys Glu Ala Lys Lys Glu Gln Lys Glu Ala Glu Lys
 755 760 765

Glu Glu Lys Glu Ala Val Lys Glu Glu Lys Lys Glu Ala Lys Glu Glu
 770 775 780

Lys Lys Ala Val Lys Asn Glu Ala Lys Lys Lys
 785 790 795

<210> 5
 <211> 3332
 <212> DNA
 <213> *Bacillus* sp. KSM-64

<400> 5		
agtacttacc attttagagt caaaagatag aagccaagca ggatttgccg atgcaaccgg	60	
cttatattta gagggaaattt ctttttaaat tgaatacgg aataaaatcag gtaaacaggt	120	
cctgattttta ttttttgaa ttttttgag aactaaagat tgaatagaa gtagaaagaca	180	
acggacataa gaaaattgta ttatgtttaa ttatagaaaa cgctttctta taattattta	240	
tacctagaac gaaaatactg tttcgaaagc ggtttactat aaaaccttat attccggctc	300	
ttttttaaa cagggggtaa aaattcactc tagtattcta atttcaacat gctataataa	360	
atttgttaga cgcaatatac atctttttt tatgatattt gtaagcggtt aaccttgc	420	
tatatgccga ttttaggaagg ggtagattt agtcaagtag tcataattta gataacttat	480	
aagttgttga gaagcaggag agaatctggg ttactcacaa gttttttaaa acattatcga	540	
aagcactttc gtttatgctt atgaattttag ctatggattt caattacttt aataatttt	600	
ggaggttaata tgatgttaag aaagaaaaca aagcaggta tttcttccat tcttatttt	660	
gttttacttc tatctttatt tccgacagct cttgcagcag aaggaaacac tcgtgaagac	720	
aattttaaac atttatttagg taatgacaat gttaaacgcc cttctgaggc tggcgcatta	780	
caattacaag aagtcgatgg acaaattgaca ttagtagatc aacatggaga aaaaattcaa	840	
ttacgtggaa tgagtacaca cggattacaa tggttccctg agatcttcaa tgataacgca	900	
tacaaagctc ttgctaacga ttggaaatca aatatgattc gtcttagctat gtatgtcggt	960	
aaaaatggct atgcttcaaa tccagagtta attaaaagca gagtcattaa aggaatagat	1020	
cttgctattt gaaatgacat gtatgtcatc gttgattggc atgtacatgc acctgggtat	1080	
ccttagagatc ccgtttacgc tggagcagaa gatttctta gagatattgc agcattat	1140	

295199US0PCT.ST25.txt

cctaacaatc cacacattat ttatgagttt gcgaatgagc caagtagtaa caataatggt	1200
ggagctggga ttccaaataa tgaagaaggt tggaaatgcgg taaaagaata cgctgatcca	1260
attgtagaaa tgttacgtga tagcgggaac gcagatgaca atattatcat tgtggtagt	1320
ccaaactgga gtcagcgtcc tgacttagca gctgataatc caattgatga tcaccataca	1380
atgtatactg ttcacttcta cactggttca catgctgctt caactgaaag ctatccgcct	1440
gaaaactccta actctgaaag aggaaacgta atgagtaaca ctcgttatgc gttagaaaac	1500
ggagtagcag tatttgcaac agagtggga actagccaag caaatggaga tggtggtcct	1560
tactttgatg aagcagatgt atggatttag tttttaaatg aaaacaacat tagctggct	1620
aactggtctt taacgaataa aaatgaagta tctggtgcatttacaccatt cgagtttaggt	1680
aagtctaacg caacaagtct tgacccaggccagaccaag tatgggtacc agaagagttt	1740
agtctttctg gagaatatgt acgtgctcgt attaaagggtt gtaactatga gccaatcgac	1800
cgtacaaaat acacgaaagt actttggac tttaatgatg gaacgaagca aggatttggaa	1860
gtgaatggag attctccagt tgaagatgta gttattgaga atgaagcggg cgctttaaaa	1920
ctttcaggat tagatgcaag taatgatgtt tctgaaggta attactgggc taatgctcgt	1980
ctttctgccc acgggtgggg aaaaagtgtt gatatttttag gtgctgaaaa acttactatg	2040
gatgtgatttggt tgatgagcc gaccacggta tcaattgctg caattccaca agggccatca	2100
gccaatttggg ttaatccaaa tcgtcaattt aagggttggc caactaattt cgtaccgttta	2160
ggagataagt ttaaagcgga attaactata acttcagctg actctccatc gttagaagct	2220
attgcgatgc atgctgaaaa taacaacatc aacaacatca ttctttttgtt aggaactgaa	2280
ggtgctgatg ttatctattt agataacattt aaagtaattt gacagaagttt gtaaattcca	2340
gttggatcatg atccaaaagg agaagctgtt cttccttctg tttttgaaga cggcacgt	2400
caagggttggg actgggttggg agagtctgggt gtgaaaacag cttaacaat tgaagaagca	2460
aacgggttcttta acgcgttatac atggaaattt ggataccag aagtaaaacc tagtgataac	2520
tgggcaacag ctccacgtt agatttctgg aaatctgact tggttcgcgg tgaaaatgtat	2580
tatgttaactt ttgatttcta tctagatcca gttcgtgcaa cagaaggcgc aatgaatatc	2640
aatttagtat tccagccacc tactaacggg tattgggtac aagcaccaaa aacgtatacg	2700
attaactttt atgaatttgc ggaagcgaat caagtaatg gtttatatca ctatgaagt	2760
aaaattaacg taagagatataccaaacattt caagatgaca cgttactacg taacatgatgt	2820
atcatttttgc cagatgtaga aagtgcattt gcagggagag tctttgtaga taatgttcgt	2880
tttgagggggg ctgctactac tgagccgggtt gaaccagagc cagttgatcc tggcgaagag	2940
acgcccgcctg tcgatgagaa ggaagcgaaa aaagaacaaa aagaagcaga gaaagaagag	3000

295199US0PCT.ST25.txt
aaagaagcag taaaagaaga aaagaaagaa gctaaagaag aaaagaaagc aatcaaaaat 3060
gaggctacga aaaaataatc taataaacta gttatagggt tatctaaagg tctgatgcag 3120
atctttaga taacctttt ttgcataact ggacatagaa tggttattaa agaaagcaag 3180
gtgttatac gatattaaaa aggtagcgat tttaaattga aaccttaat aatgtttgt 3240
gatagaatga tgaagtaatt taagaggggg aaacgaagtg aaaacggaaa tttctagtag 3300
aagaaaaaca gaccaagaaa tactgcaagc tt 3332

<210> 6
<211> 793
<212> PRT
<213> *Bacillus* sp. KSM-64

<400> 6

Ala Glu Gly Asn Thr Arg Glu Asp Asn Phe Lys His Leu Leu Gly Asn
1 5 10 15

Asp Asn Val Lys Arg Pro Ser Glu Ala Gly Ala Leu Gln Leu Gln Glu
20 25 30

Val Asp Gly Gln Met Thr Leu Val Asp Gln His Gly Glu Lys Ile Gln
35 40 45

Leu Arg Gly Met Ser Thr His Gly Leu Gln Trp Phe Pro Glu Ile Leu
50 55 60

Asn Asp Asn Ala Tyr Lys Ala Leu Ala Asn Asp Trp Glu Ser Asn Met
65 70 75 80

Ile Arg Leu Ala Met Tyr Val Gly Glu Asn Gly Tyr Ala Ser Asn Pro
85 90 95

Glu Leu Ile Lys Ser Arg Val Ile Lys Gly Ile Asp Leu Ala Ile Glu
100 105 110

Asn Asp Met Tyr Val Ile Val Asp Trp His Val His Ala Pro Gly Asp
115 120 125

Pro Arg Asp Pro Val Tyr Ala Gly Ala Glu Asp Phe Phe Arg Asp Ile
130 135 140

Ala Ala Leu Tyr Pro Asn Asn Pro His Ile Ile Tyr Glu Leu Ala Asn
145 150 155 160

Glu Pro Ser Ser Asn Asn Asn Gly Gly Ala Gly Ile Pro Asn Asn Glu
165 170 175

295199US0PCT.ST25.txt

Glu Gly Trp Asn Ala Val Lys Glu Tyr Ala Asp Pro Ile Val Glu Met
180 185 190

Leu Arg Asp Ser Gly Asn Ala Asp Asp Asn Ile Ile Ile Val Gly Ser
195 200 205

Pro Asn Trp Ser Gln Arg Pro Asp Leu Ala Ala Asp Asn Pro Ile Asp
210 215 220

Asp His His Thr Met Tyr Thr Val His Phe Tyr Thr Gly Ser His Ala
225 230 235 240

Ala Ser Thr Glu Ser Tyr Pro Pro Glu Thr Pro Asn Ser Glu Arg Gly
245 250 255

Asn Val Met Ser Asn Thr Arg Tyr Ala Leu Glu Asn Gly Val Ala Val
260 265 270

Phe Ala Thr Glu Trp Gly Thr Ser Gln Ala Asn Gly Asp Gly Gly Pro
275 280 285

Tyr Phe Asp Glu Ala Asp Val Trp Ile Glu Phe Leu Asn Glu Asn Asn
290 295 300

Ile Ser Trp Ala Asn Trp Ser Leu Thr Asn Lys Asn Glu Val Ser Gly
305 310 315 320

Ala Phe Thr Pro Phe Glu Leu Gly Lys Ser Asn Ala Thr Ser Leu Asp
325 330 335

Pro Gly Pro Asp Gln Val Trp Val Pro Glu Glu Leu Ser Leu Ser Gly
340 345 350

Glu Tyr Val Arg Ala Arg Ile Lys Gly Val Asn Tyr Glu Pro Ile Asp
355 360 365

Arg Thr Lys Tyr Thr Lys Val Leu Trp Asp Phe Asn Asp Gly Thr Lys
370 375 380

Gln Gly Phe Gly Val Asn Gly Asp Ser Pro Val Glu Asp Val Val Ile
385 390 395 400

Glu Asn Glu Ala Gly Ala Leu Lys Leu Ser Gly Leu Asp Ala Ser Asn
405 410 415

Asp Val Ser Glu Gly Asn Tyr Trp Ala Asn Ala Arg Leu Ser Ala Asp
420 425 430

295199US0PCT.ST25.txt

Gly Trp Gly Lys Ser Val Asp Ile Leu Gly Ala Glu Lys Leu Thr Met
435 440 445

Asp Val Ile Val Asp Glu Pro Thr Thr Val Ser Ile Ala Ala Ile Pro
450 455 460

Gln Gly Pro Ser Ala Asn Trp Val Asn Pro Asn Arg Ala Ile Lys Val
465 470 475 480

Glu Pro Thr Asn Phe Val Pro Leu Gly Asp Lys Phe Lys Ala Glu Leu
485 490 495

Thr Ile Thr Ser Ala Asp Ser Pro Ser Leu Glu Ala Ile Ala Met His
500 505 510

Ala Glu Asn Asn Asn Ile Asn Asn Ile Ile Leu Phe Val Gly Thr Glu
515 520 525

Gly Ala Asp Val Ile Tyr Leu Asp Asn Ile Lys Val Ile Gly Thr Glu
530 535 540

Val Glu Ile Pro Val Val His Asp Pro Lys Gly Glu Ala Val Leu Pro
545 550 555 560

Ser Val Phe Glu Asp Gly Thr Arg Gln Gly Trp Asp Trp Ala Gly Glu
565 570 575

Ser Gly Val Lys Thr Ala Leu Thr Ile Glu Glu Ala Asn Gly Ser Asn
580 585 590

Ala Leu Ser Trp Glu Phe Gly Tyr Pro Glu Val Lys Pro Ser Asp Asn
595 600 605

Trp Ala Thr Ala Pro Arg Leu Asp Phe Trp Lys Ser Asp Leu Val Arg
610 615 620

Gly Glu Asn Asp Tyr Val Thr Phe Asp Phe Tyr Leu Asp Pro Val Arg
625 630 635 640

Ala Thr Glu Gly Ala Met Asn Ile Asn Leu Val Phe Gln Pro Pro Thr
645 650 655

Asn Gly Tyr Trp Val Gln Ala Pro Lys Thr Tyr Thr Ile Asn Phe Asp
660 665 670

Glu Leu Glu Glu Ala Asn Gln Val Asn Gly Leu Tyr His Tyr Glu Val

295199US0PCT.ST25.txt
680 685

Lys Ile Asn Val Arg Asp Ile Thr Asn Ile Gln Asp Asp Thr Leu Leu
 690 695 700

Arg Asn Met Met Ile Ile Phe Ala Asp Val Glu Ser Asp Phe Ala Gly
 705 710 715 720

Arg Val Phe Val Asp Asn Val Arg Phe Glu Gly Ala Ala Thr Thr Glu
 725 730 735

Pro Val Glu Pro Glu Pro Val Asp Pro Gly Glu Glu Thr Pro Pro Val
 740 745 750

Asp Glu Lys Glu Ala Lys Lys Glu Gln Lys Glu Ala Glu Lys Glu Glu
 755 760 765

Lys Glu Ala Val Lys Glu Glu Lys Lys Glu Ala Lys Glu Glu Lys Lys
 770 775 780

Ala Ile Lys Asn Glu Ala Thr Lys Lys
 785 790

<210> 7
<211> 572
<212> DNA
<213> *Bacillus* sp. KSM-S237

<400> 7 gat~~tt~~gccga tgcaacag~~gc~~ ttat~~at~~ttag aggaaat~~tc~~ tttt~~aa~~att gaatacg~~ga~~ 60
taaaat~~c~~cagg taaacagg~~tc~~ ctgat~~ttt~~at tttt~~t~~gagt tttt~~ag~~aga actgaag~~at~~ 120
gaaataaaag tagaagacaa aggacataag aaaatt~~gc~~at tagttt~~ta~~at tatagaaaac 180
gc~~ttt~~at aattat~~ttt~~at ac~~t~~agaac~~g~~ aaaatact~~gt~~ ttc~~gaa~~ag~~cg~~ gtt~~t~~actata 240
aaac~~ctt~~tata ttccggct~~ct~~ tttt~~aa~~ac aggggt~~aa~~ aatt~~c~~act~~ct~~ agtatt~~ct~~aa 300
ttt~~c~~acat~~g~~ ctataataaa tt~~t~~gtaagac gcaat~~at~~gca tct~~ttt~~tt tacgatata~~t~~ 360
gtaagcg~~gtt~~ aac~~ctt~~gt~~gc~~ tata~~tg~~ccga tt~~t~~taggaagg ggg~~gt~~agaat attt~~ca~~ag~~ta~~ 420
gtaataacat acaataactta taagtt~~gtt~~g agaagcag~~ga~~ gagcatct~~gg~~ gtt~~t~~actcaca 480
agtttttta aaactttaac gaaagcactt tc~~gg~~taat~~gc~~ ttat~~g~~aattt agctatt~~tg~~a 540
tt~~c~~aatttact ttaaaaat~~at~~ ttaggag~~gt~~a at 572

<210> 8
<211> 609
<212> DNA
<213> *Bacillus* sp. KSM-64

295199US0PCT.ST25.txt

<400> 8
agtacttacc attttagagt caaaagatag aagccaagca ggatttgccg atgcaaccgg 60
cttataattta gagggaaattt ctttttaaat tgaatacgg aataaaatcgat gtaaaacaggt 120
cctgattttta ttttttgaa ttttttgag aactaaagat tgaaatagaa gtagaaagaca 180
acggacataa gaaaattgta ttagtttaa ttatagaaaa cgctttctta taattattta 240
tacctagaac gaaaatactg tttcgaaagc ggtttactat aaaaaccttat attccggctc 300
tttttttaaa caggggggtga aaattcactc tagtattcta atttcaacat gctataataa 360
atttgtttaa gcaatataac atctttttt tatgatattt gtaagcggtt aaccttgc 420
tatatgccga ttttaggaagg gggtagaata tttcaagtag taataacata caataacttat 480
aagttgttga gaagcaggag agaatctggg ttactcacaa gttttttaaa acattatcga 540
aagcactttc gtttatgctt atgaatttag ctatttgatt caattacttt aataattttta 600
ggaggtaat 609

<210> 9
<211> 37
<212> DNA
<213> Artificial sequence

<220>
<223> Oligonucleotide as PCR primer designed from nucleotide sequence
of *Bacillus* sp. KSM-S237 gene for cellulase; the sequence with a
insertion of the BamHI restriction site at the 5'-end

<400> 9
ttgcggatcc aacaggctta tatttagagg aaatttc 37

<210> 10
<211> 40
<212> DNA
<213> Artificial sequence

<220>
<223> Oligonucleotide as PCR primer designed from nucleotide sequence
of *Bacillus* sp. KSM-S237 gene for cellulase; the sequence
containing eight nucleotides substitution for SigmaE recognition

<400> 10
gtatgttatt actacttgaa atattctacc ccccttccta 40

<210> 11
<211> 39
<212> DNA
<213> Artificial sequence

<220>
<223> Oligonucleotide as PCR primer designed from nucleotide sequence
of *Bacillus* sp. KSM-S237 gene for cellulase; the sequence
containing eight nucleotides substitution for SigmaE recognition

<400> 11

atatttcaag tagtaataac atacaatact tataagttg

<210> 12

<211> 20

<212> DNA

<213> Artificial sequence

<220>

<223> Oligonucleotide as PCR primer designed from nucleotide sequence
of *Bacillus* sp. KSM-S237 gene for cellulase

<400> 12

tcgctaccct tttattatcg

20

<210> 13

<211> 1795

<212> DNA

<213> *Bacillus* sp. KSM-K38

<400> 13

caggccagcc aaagtagccca ccaactaagt aacatcgatt caggataaaa gtagcgaaa	60
cgtgcgcaa aactgcgcaa ctactagcac tcttcagggc ctaaaccacc tttttccaa	120
aaatgacatc atataaacaa atttgtctac caatcaactat ttaaagctgt ttatgatata	180
tgtaaacgtt atcattaaaaa ggaggatttt gatgagaaga tggtagtagt caatgttgc	240
agtgttattt ttatttcctt cggttagtgc tgcagatggc ttgaacggta cgtatgtca	300
gtattatgag tggcatttgg aaaacgacgg gcagcattgg aatcggttgc acgtatgtgc	360
cgcagctttg agtgatgctg gtattacagc tattttggatt ccgccagcct acaaaggtaa	420
tagtcaggcg gatgttgggt acgggtcata cgatcttat gatttaggag agttcaatca	480
aaagggtact gttcgaacga aatacggAAC taaggcacag cttgaacggag ctattgggtc	540
ccttaaatct aatgatatacgt atgtatacgg agatgtcgatc atgaatcata aaatgggagc	600
tgattttacg gaggcagtgc aagctgttca agtaaatcca acgaatcggtt ggcaggatata	660
ttcaggtgcc tacacgatttgc atgcgtggac gggtttcgac ttttcagggc gtaacaacgc	720
ctattcagat tttaagtggc gatggttcca tttaatgggt gttgactggg atcagcgctc	780
tcaagaaaaat catattttcc gctttgcaaa tacgaactgg aactggcgag tggatgaaga	840
gaacggtaat tatgattacc tggtaggatc gaatatcgac ttttagtcatc cagaagtaca	900
agatgagttt aaggattttgg gtagctgggtt taccgtatgg ttagattttgg atggttatcg	960
tttagatgtt attaaacata ttccattctg gtatacatct gattgggttc ggcattcagcg	1020
caacgaagca gatcaagatt tatttgcgtt agggaaatat tggaaaggatg acgttaggtgc	1080
tctcgaattt tatttagatg aaatgaatttgg gtagatgtct ctattcgtatc ttccactaa	1140
ttataatttt taccgggctt cacaacaagg tggaaagctat gatatgcgtat atattttacg	1200
aggatcttta gtagaagcgc atccgatgca tgcagttacg tttgttgcata atcatgatac	1260

295199US0PCT.ST25.txt

tcagccaggg gagtcattag agtcatgggt tgctgattgg tttaagccac ttgcttatgc	1320
gacaattttg acgcgtgaag gtggttatcc aaatgtattt tacggtgatt actatggat	1380
tcctaacgt aacatttcag ctaaaaaaga tatgattgat gagctgcttgc acgtca	1440
aaattacgca tatggcacgc agcatgacta ttttgcattcat tggatgttgc tagatggac	1500
taggaaagga tcttcctcca gacctaattc aggcccttgcg actattatgt cgaatggacc	1560
tgggtttcc aagtggatgt atgttggac tcagaatgca ggacaaacat ggacagattt	1620
aactggtaat aacggagcgt ccgttacaat taatggcgat ggatggggcg aattctttac	1680
aatggagga tctgtatccg tgtacgtgaa ccaataacaa aaagccttga gaaggattc	1740
ctccctaact caaggcttcc tttatgtcgc ttagctttac gcttctacga ctttg	1795

<210> 14

<211> 480

<212> PRT

<213> *Bacillus* sp. KSM-K38

<400> 14

Asp Gly Leu Asn Gly Thr Met Met Gln Tyr Tyr Glu Trp His Leu Glu
 1 5 10 15

Asn Asp Gly Gln His Trp Asn Arg Leu His Asp Asp Ala Ala Ala Leu
 20 25 30

Ser Asp Ala Gly Ile Thr Ala Ile Trp Ile Pro Pro Ala Tyr Lys Gly
 35 40 45

Asn Ser Gln Ala Asp Val Gly Tyr Gly Ala Tyr Asp Leu Tyr Asp Leu
 50 55 60

Gly Glu Phe Asn Gln Lys Gly Thr Val Arg Thr Lys Tyr Gly Thr Lys
 65 70 75 80

Ala Gln Leu Glu Arg Ala Ile Gly Ser Leu Lys Ser Asn Asp Ile Asn
 85 90 95

Val Tyr Gly Asp Val Val Met Asn His Lys Met Gly Ala Asp Phe Thr
 100 105 110

Glu Ala Val Gln Ala Val Gln Val Asn Pro Thr Asn Arg Trp Gln Asp
 115 120 125

Ile Ser Gly Ala Tyr Thr Ile Asp Ala Trp Thr Gly Phe Asp Phe Ser
 130 135 140

295199US0PCT.ST25.txt

Gly Arg Asn Asn Ala Tyr Ser Asp Phe Lys Trp Arg Trp Phe His Phe
145 150 155 160

Asn Gly Val Asp Trp Asp Gln Arg Tyr Gln Glu Asn His Ile Phe Arg
165 170 175

Phe Ala Asn Thr Asn Trp Asn Trp Arg Val Asp Glu Glu Asn Gly Asn
180 185 190

Tyr Asp Tyr Leu Leu Gly Ser Asn Ile Asp Phe Ser His Pro Glu Val
195 200 205

Gln Asp Glu Leu Lys Asp Trp Gly Ser Trp Phe Thr Asp Glu Leu Asp
210 215 220

Leu Asp Gly Tyr Arg Leu Asp Ala Ile Lys His Ile Pro Phe Trp Tyr
225 230 235 240

Thr Ser Asp Trp Val Arg His Gln Arg Asn Glu Ala Asp Gln Asp Leu
245 250 255

Phe Val Val Gly Glu Tyr Trp Lys Asp Asp Val Gly Ala Leu Glu Phe
260 265 270

Tyr Leu Asp Glu Met Asn Trp Glu Met Ser Leu Phe Asp Val Pro Leu
275 280 285

Asn Tyr Asn Phe Tyr Arg Ala Ser Gln Gln Gly Gly Ser Tyr Asp Met
290 295 300

Arg Asn Ile Leu Arg Gly Ser Leu Val Glu Ala His Pro Met His Ala
305 310 315 320

Val Thr Phe Val Asp Asn His Asp Thr Gln Pro Gly Glu Ser Leu Glu
325 330 335

Ser Trp Val Ala Asp Trp Phe Lys Pro Leu Ala Tyr Ala Thr Ile Leu
340 345 350

Thr Arg Glu Gly Gly Tyr Pro Asn Val Phe Tyr Gly Asp Tyr Tyr Gly
355 360 365

Ile Pro Asn Asp Asn Ile Ser Ala Lys Lys Asp Met Ile Asp Glu Leu
370 375 380

Leu Asp Ala Arg Gln Asn Tyr Ala Tyr Gly Thr Gln His Asp Tyr Phe
385 390 395 400

295199US0PCT.ST25.txt

Asp His Trp Asp Val Val Gly Trp Thr Arg Glu Gly Ser Ser Ser Arg
405 410 415

Pro Asn Ser Gly Leu Ala Thr Ile Met Ser Asn Gly Pro Gly Gly Ser
420 425 430

Lys Trp Met Tyr Val Gly Arg Gln Asn Ala Gly Gln Thr Trp Thr Asp
435 440 445

Leu Thr Gly Asn Asn Gly Ala Ser Val Thr Ile Asn Gly Asp Gly Trp
450 455 460

Gly Glu Phe Phe Thr Asn Gly Gly Ser Val Ser Val Tyr Val Asn Gln
465 470 475 480

<210> 15

<211> 25

<212> DNA

<213> Artificial sequence

<220>

<223> Oligonucleotide as PCR primer designed from nucleotide sequence
of *Bacillus* sp. KSM-S237 gene for cellulase; the sequence with a
insertion of the BamHI restriction site at the 5'-end

<400> 15

cccgatcca acaggcttat attta

25

<210> 16

<211> 29

<212> DNA

<213> Artificial sequence

<220>

<223> Oligonucleotide as PCR primer; its 3'-portion designed from
nucleotide sequence of *Bacillus* sp. KSM-S237 gene for cellulase
and its 5'-portion designed from nucleotide sequence of *Bacillus*
sp. KSM-K38 gene for amylase

<400> 16

ttcaatccat ctgctgcaag agctgccgg

29

<210> 17

<211> 30

<212> DNA

<213> Artificial sequence

<220>

<223> Oligonucleotide as PCR primer; its 3'-portion designed from nucle
otide sequence of *Bacillus* sp. KSM-K38 gene for amylase and its
5'-portion designed from nucleotide sequence of *Bacillus* sp.
KSM-S237 gene for cellulase

<400> 17

gctttgcag cagatggatt gaacggtagc

30

<210> 18
<211> 30
<212> DNA
<213> Artificial sequence

<220>
<223> Oligonucleotide as PCR primer designed from nucleotide sequence of *Bacillus* sp. KSM-K38 gene for amylase; the sequence with a insertion of the *Xba*I restriction site at the 5'-end

<400> 18 30
ttggctctaga ccccaagctt caaagtgcgt

<210> 19
<211> 27
<212> DNA
<213> Artificial sequence

<220>
<223> A promoter sequence recognized by *SigE*

<400> 19 27
atatttcaag tagtaataac atacaat

<210> 20
<211> 27
<212> DNA
<213> Artificial sequence

<220>
<223> Original sequence in an alkaline cellulase gene

<400> 20 27
ttgagtcaag tagtaataat atagata